



lalign output for SEQ ID 2 vs. SEQ ID 14

[ISREC-Server] Date: Tue Jan 25 17:25:30 Europe/Zurich 2005

LALIGN finds the best local alignments between two sequences version 2.0u66 September 1998 Please cite: X. Huang and W. Miller (1991) Adv. Appl. Math. 12:373-381

Comparison of:

(A) ./wwtmp/lalign/.18855.1.seq SEQ ID 2

(B) ./wwtmp/lalign/.18855.2.seq SEQ ID 14

using matrix file: BL50, gap penalties: -14/-4

61.1% identity in 108 aa overlap; score: 456 E(10,000): 7.4e-34

	10	20	30	40	50	60
SEQ	LHGS	SGNE	IEGP	QNA	TVL	KGS
	:	:	:	:	:
SEQ	LTAS	GSS	YQI	IEGP	QNV	TVL
	20	30	40	50	60	70
	70	80	90	100	110	
SEQ	RFTS	QRYD	QGGN	FTSEM	IIHN	VEPS
	:::	:	:	:
SEQ	RFTY	ASYN	STDS	FI	SELI	IIHD
	80	90	100	110	120	

53.3% identity in 92 aa overlap; score: 290 E(10,000): 4.5e-19

	300	310	320	330	340	350
SEQ	KKSE	KEKT	NK---	ETET	ESGN	ENSG

SEQ	RKSAN	MRTN	KADP	ETKL	KSGK	ENYGY
	140	150	160	170	180	190
	360	370	380			
SEQ	QRAD	QRPP	RPA	SH	PQAS	FN
	:	:	:	:
SEQ	QELN	KHQ	PGP	ATH	PRV	SF
	200	210	220			

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lalign output for SEQ ID 4 vs. SEQ ID 14

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LALIGN finds the best local alignments between two sequences version 2.0u66 September 1998 Please cite: X. Huang and W. Miller (1991) Adv. Appl. Math. 12:373-381

Comparison of:

(A) ./wwtmp/lalign/.19190.1.seq SEQ ID 4

(B) ./wwtmp/lalign/.19190.2.seq SEQ ID 14

using matrix file: BL50, gap penalties: -14/-4

61.0% identity in 105 aa overlap; score: 447 E(10,000): 4.8e-33

	20	30	40	50	60	70
SEQ	SGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALS DMVVL SVRPM EPIITNDRFT					

SEQ	SGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLT TQGPIITNNRFT					
	30	40	50	60	70	80

	80	90	100	110
SEQ	SQRYDQGGNFTSEMI IHNVEPSDSGNIRCSLQNSRLHGSAYLTVQ			

SEQ	YASYNSTDSFISELIIHDVQPSDSG SVQCSLQNSHGFGSAFLSVQ			
	90	100	110	120

53.3% identity in 92 aa overlap; score: 290 E(10,000): 4.5e-19

	300	310	320	330	340	350
SEQ	KKSEKEKTNK---ETETESGNENSGYNSDEQKTTDTASLPPKSCSSDPEQRNSSCGPPH					

SEQ	RKSANMRTNKADPETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PY					
	140	150	160	170	180	190

	360	370	380
SEQ	QRADQRPPRPASHPQASFNLASPEKVSNTTVV		

SEQ	QELNKHQPGPATHPRVSFDIASPQKVRNVTLV		
	200	210	220

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Comparison of:

(B) ./wwtmp/lalign/.19757.2.seq SEO ID 14

using matrix file: BL50, gap penalties: -14/-4

57.9% identity in 114 aa overlap; score: 458 E(10,000): 5e-34

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      10      20      30      40      50      60
SEQ  LLTVPEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSPRME
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : .
SEQ  LVILAQLTASGSSYQIIIEGPQNVTVLKDEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQG
      20      30      40      50      60      70

      70      80      90      100     110
SEQ  PIITNDRFTSQRYDQGGNFTSEMIIHNVESDSGNIRCSLQNSRLHGSAYLTVQ
      : : : : : . . : : : : : : : : : : : : : : : : : : : :
SEQ  PIITNNRFTYASYNSTDSFISELIIHDVQPSDSGVSQCQLQNSHGFGSAFLSVQ
      80      90      100     110     120

```

53.3% identity in 92 aa overlap; score: 292 E(10,000): 3e-19

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300          310          320          330          340          350
SEQ  KKSEKEKTNK--ETETESGNGNSGYNSDEQKTTTETASLPPKSCSSDPEQRNSSCGPPH
    .:: . .:::  ::. .:::  :::  :::  :::  :::  :::  :::  :::  :::  :::
SEQ  RKSANMRTNKADPETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLEPEKRSSSL--PY
      140      150      160      170      180      190

      360      370      380
SEQ  QRADQRPPRPASHPQASFNLASPEKVSNTTVV
    . . . : :::::::::::::::::::: :::
SEQ  QELNKHQPGPATHPRVSFDIASPQKVRNVTLV
      200      210      220

```

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